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Enhancing Genetic Gain in Potato Clones through Phenotyping Late Blight Resistance

Subash Subedi[1]*, Niru Tripathi[2], Saraswati Neupane[3], and Puja Bastakoti[4]

[1]Nepal Agricultural Research Council, Hill Crops Research Program, Kabre, Dolakha, Nepal
[2]Nepal Agricultural Research Council, National Potato Research Program, Khumaltar, Lalitpur, Nepal
[3]Nepal Agricultural Research Council, National Maize Research Program, Rampur, Chitawan, Nepal
[4]Nepal Polytechnic Institute, Purbanchal University, Bhojad, Chitawan, Nepal

Abstract. Late blight, caused by *Phytophthora infestans* (Mont.) de Bary, is a devastating disease of potato (*Solanum tuberosum* L.). To identify potential sources of resistance to the disease, 32 clones received from the National Potato Research Program (NPRP) were evaluated under natural conditions at the National Maize Research Program Rampur, Chitwan in 2018 and 2019. Potato cultivars Desire, Kufri Jyoti, and Farmers local were used as moderately resistant, susceptible, and highly susceptible checks, respectively. The experiments were laid out in α-lattice design with two replications. Each experimental plot of 3.6 m^2 was seeded as two 3m long rows with 0.6 and 0.25 m row and plant spacing, respectively. Agronomic practices were followed as recommended by NPRP. The disease severity was measured based on a percentage of leaf area infected using disease scale of (1 to 9) at three times in seven days intervals. Disease severity values were converted into the area under disease progress curve (AUDPC). During harvest, the total yield and its components were recorded. Potato clones differed significantly ($P \leq 0.01$) for disease severity, yield, and yield components. The results revealed high genetic variability, heritability, and genetic gain for disease parameters, tuber yield, and its components. Six clones (CIP311622.9, PRP277072.122, PRP146971.135, PRP147072.27, CIP311350.27, and PRP146971.117 had lower area under disease progress curve AUDPC) values (274.25 to 421.03), showed higher resistant in both years and yielded more tuber yield (~20 t/ha) than other clones. These clones could be used to develop late blight resistant, high yielding potato varieties.

Keywords: genetic gain, late blight, phenotyping, potato, resistance

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1. Introduction

Potato is a successful crop in enabling smallholder farmers to achieve food security and tackle poverty with the most diverse distribution patterns globally [1] and is predominantly cultivated in places where poverty, starvation, and malnutrition are all quite high. After wheat and rice, the potato is currently the world's third-largest staple food for human consumption [2], despite the fact that a major percentage of potato products are utilized for seed and animal feed. Potato is

*Corresponding author at: Nepal Agricultural Research Council, Hill Crops Research Program, Kabre, Dolakha, Nepal

E-mail address: subedi.subash1@gmail.com

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mostly produced as a cash crop and is a significant source of revenue in Nepal. The crop is grown during winter season, either as a monoculture or in combination with maize, wheat, or rice. Recent statistics showed that potatoes are currently being grown on an estimated 193,997 hectares in Nepal with a production of about 3,112,947 mt [3]. The current national yield of potato in Nepal is about 16.05 t/ha [3] which is very low as compared to the attainable yield and yield of neighboring countries due to various biotic, abiotic, and socio-economic constraints. Potatoes face high production losses caused mainly by a diversity of pests and diseases. Potato crop can be harmed by about 160 diseases and disorders. Among these, 50 of which are caused by fungi, 10 by bacteria, 40 by viruses, and others by non-parasitic diseases [4]. Among fungi, late blight caused due to oomycete fungi *Phytophthora infestans* (Mont.) de Bary, represents the most devastating disease for potato worldwide. High levels of moisture are necessary for the lesion development and infection. Thus, the disease will spread rapidly, infects vegetative tissues, and kill the plant in a couple of days [5]. The pathogen feeds on the dying, necrotized cells, and in high humidity, white mildew growth appears on the leaves, reflecting sporangiophores and sporangia that arise through the stomata [6]. A large number of genes involved in pathogenicity, calcium signaling, and metabolism are either up-regulated or transcribed in waves during spore development and germination [7], while fatty acid biosynthesis genes are down-regulated [8]. This pathogen can cause annual losses of 16% of the global potato production [9]. The incidence of late blight is expected to accelerate globally under highly unpredictable weather conditions, mainly affecting the range of cultivated areas in developing countries [10].

Chemical fungicides are still the most often used method for late blight management, making late blight one of the world's major drivers of pesticide usage. Every year, the need for weekly fungicide treatments generates a billion-dollar market globally [9]. The widespread use of pesticides in potatoes is a major source of worry for both humans and the environment, and it must be addressed via the development and more thorough application of Integrated Pest Management (IPM) techniques. The application of host resistance is the most successful strategy for combating late blight. The advent of early and high-yielding varieties resistant to *P. infestans* has been a long-standing aim of potato breeding. Late blight may be handled with less fungicide utilizing genetic resistance, either by reducing the fungicide dose or by using longer treatment intervals [11]–[15]. The adoption of resistant cultivars might considerably minimize late blight losses, particularly in developing nations such as Nepal. Although the use of resistant varieties is considered to be an innovative approach to late blight disease management, planting susceptible varieties are still practiced by many wholesalers and processing industries, resource-poor farmers [16]. The inclusion of a wider range of genetic resistance in disease control strategies reduces the usage of fungicides, lowers production costs, and reduces harm to human health and the environment.

The main objective of the present study was to evaluate and identify sources of late blight resistance in potato clones and to contribute genetic gain in tuber yield and its components in the terai area of Nepal.

2. Materials and Methods

2.1. Potato Cultivars and Planting

Thirty-two clones developed by International Potato Center (IPC) and Potato Research Program (PRP) were received from the National Potato Research Program, Khumaltar, Nepal. Desire (moderately resistant), Kufri Jyoti (susceptible) and Farmers local (highly susceptible) were used checks and screened at the National Maize Research Program Rampur, Chitwan during the winter season for two consecutive years 2018 and 2019 under natural epiphytotic conditions. The research area is located at $27^0$37' N latitude and $84^0$25' E longitude, at an altitude of 256 masl, and has a subtropical climate. The experiments were laid out in α-lattice design with two replications in two consecutive years. Each experimental plot of 3.6 m^2 was seeded as two 3m long rows with 0.6 and 0.25 m row and plant spacing, respectively. As a baseline dosage, plant nutrients in the form of N, P_20_5, and K_20 (100:100:60 kg NPK/ha) were placed to the furrows and filled with soil via urea, di-ammonium phosphate, murate of potash, and compost at 20 t/ha. Sprouted potato seed tubers of about same physiological age were planted in ridges at a depth of 5-6 cm. Irrigation was provided at 40 and 60 days after planting followed by two manual weeding and earthing up.

2.2. Disease Assessment

Disease severity was measured in percentage basis following the initial appearance of disease in the plot, three times at seven-day intervals, using a disease scale ranging from 1 to 9 [17]. Disease severity was converted into the area under disease progress curve (AUDPC) according to [18]. The relative AUDPC (rAUDPC) was also calculated as per [19]. All accessions were classified into five groups highly resistant (HR), resistant (R), moderately resistant (MR), susceptible (S), and highly susceptible (HS). Based on pooled mean AUDPC values < 250 were grouped into highly resistant: 250 to 450 = resistant, 451 to 650 = moderately resistant, 651 to1200 = susceptible and >1200 = highly susceptible.

2.3. Yield and Agronomic Assessment

Total yield was calculated from the net harvested area (3.6 m^2) at the time of harvesting for each trial plot. Tubers were cleaned well, and each grade was weighed individually from each plot. Each net plot's tuber weight was calculated. The data were then converted in tons per hectare (t/ha). Data related to leaf length (cm), leaf width (cm), plant height (cm), and main stem/plant were recorded during peak vegetative stage of the crop.

2.4. Data Analysis

Data for AUDPC, disease score, severity, intensity, and yield parameters were subjected to analysis of variance (ANOVA). The phenotypic and genotypic variance and coefficients of variation were estimated according to the methods suggested by [20]. Heritability (H^2) in a broad sense was computed using the formula described previously [21], [22] Genetic advance (GA) for each trait was computed using the formula of [21], [23]. Phenotypic and genotypic correlations between tuber yield and genotype resistance traits were estimated using the method described previously [24]. Genotypic and phenotypic correlation coefficients between disease parameters, yield, and yield components in potato clones were computed to obtain better estimates of the associations between tuber yield and disease resistance. Analyses of variance were performed for each trait for each year and combined to detect differences among the potato clones using META-R software developed by CIMMYT [25].

3. Results and Discussion

The analysis of variance revealed highly significant ($P < 0.01$) differences among the 32 clones for all the recorded traits during the winter season of 2018 and 2019 (Table 1).

Table 1. Descriptive Statistics of Potato Clones for the Traits Recorded During Two Consecutive Years at Rampur, Chitwan, Nepal

Traits	Year 2018				Year 2019			
	Mean ± SEm	Range	Sig.	CV %	Mean ± SEm	Range	Sig.	CV %
PDI% (55 DAP)	†30.72 ± 1.83	12.15 - 67.45	**	4.86	34.37 ± 2.43	11.08 -74.37	**	4.75
PDI% (62 DAP)	48.30 ± 2.38	16.25 - 78.95	**	3.16	48.96 ± 3.17	12.21 - 99.90	**	3.29
PDI% (69 DAP)	67.29 ± 3.09	23.25 - 97.65	**	1.77	65.80 ± 3.46	21.08 - 99.90	**	1.79
AUDPC	875.73 ± 41.91	331.20 - 1398.15	**	2.10	693.30 ± 41.13	205.91 - 1289.82	**	1.89
DI %	67.56 ± 2.84	22.64 - 97.35	**	2.25	68.52 ± 2.96	13.64 - 96.00	**	5.17
Leaf length (cm)	5.86 ± 0.15	3.95 - 7.95	**	2.11	5.81 ± 0.13	3.95 - 7.80	**	2.09
Leaf width (cm)	3.88 ± 0.11	2.45 - 5.65	**	2.94	3.83 ± 0.09	2.65 - 5.50	**	2.82
Plant height (cm)	24.26 ± 0.99	11.45 - 42.35	**	5.06	24.32 ± 0.91	11.60 - 46.15	**	8.14
Main stem/plant	4.27 ± 0.17	2.15 - 9.75	**	2.64	4.14 ± 0.17	1.80 - 9.70	**	4.75
Yield (t/ha)	9.83 ± 1.06	1.42 - 30.72	**	10.45	9.26 ± 1.07	0.80 - 29.11	**	12.18

Note: †means of two replications, **- significant at ≤ 0.01 p level, Sig = significance; SEm = standard error mean; CV = coefficient of variation; PDI = percent disease index; DAP = days after planting; AUDPC = area under disease progress curve; DI = disease incidence; cm = centimeter; % = percentage, t/ha = ton per hectare

This showed that there was enough diversity in the genotypes to allow for the selection of better and desired clones for future development. Range, mean, and standard error were computed to evaluate the degree of existing variability in the current clones (Table 1-2). The range, on the other hand, is a basic way of estimating variability that simply shows observed phenotypic variability. The AUDPC was ranged between 205.91 to 1398.15 with the mean value of 784.52 ±

30.34. Similarly, the yield of of tuber was ranged between 0.80 to 30.72 t/ha with the mean yield of 9.54 ± 0.75 t/ha (Table 2). It also showed within range of co-efficient of variation for all the traits. The phenotypic variants for all of the characteristics were larger than the genotypic variations (Table2), presumably due to a non-genetic factor that played a major role in the expression of these features. The characteristics with the highest phenotypic and genotypic variations were tuber yield, Percent Disease Index (PDI), AUDPC, and Disease Incidence (DI) (Table 2).

Table 2. Variation, Heritability, and Genetic Advance in Potato Clones for Late Blight Disease and Yield Traits during 2018-2019 at Rampur, Chitwan, Nepal

Traits	Mean ± SEm	Range	PCV (%)	GCV (%)	H^2B	GA (5%)	GA (% of mean)
PDI% (55 DAP)	32.54 ± 1.53	11.08 – 74.37	50.48	50.24	0.94	31.85	97.88
PDI% (62 DAP)	48.63 ± 1.98	12.21 – 99.90	43.38	43.27	0.93	40.41	83.11
PDI% (69 DAP)	66.55 ± 2.31	21.08 – 99.90	39.07	39.03	0.98	52.65	79.12
AUDPC	784.52 ± 30.34	205.91 – 1398.15	41.39	41.34	0.97	648.03	82.60
DI %	68.04 ± 2.04	13.64 – 97.35	33.89	33.68	0.98	46.69	68.62
Leaf length (cm)	5.83 ± 0.10	3.95 – 7.95	18.45	18.32	0.97	2.15	36.85
Leaf width (cm)	3.85 ± 0.07	2.45 – 5.65	20.18	19.97	0.96	1.53	39.72
Plant height (cm)	24.29 ± 0.67	11.45 – 46.15	31.08	30.35	0.98	15.19	62.54
Main stem/plant	4.21 ± 0.12	1.80 – 9.75	31.21	30.97	0.97	2.63	62.42
Yield (t/ha)	9.54 ± 0.75	0.80 – 30.72	88.52	87.72	0.98	17.05	178.70

Note: SEm = standard error mean; PCV = phenotypic coefficient of variation; GCV = genotypic coefficient of variation; H^2B = Broad sense heritability; GA (5%) = genetic advance at 5% selection intensity; CV = coefficient of variation; PDI = percent disease index; DAP = days after planting; AUDPC = area under disease progress curve; DI = disease incidence; cm = centimeter; % = percentage; t/ha = ton per hectare

The phenotypic coefficient of variation has a greater numerical value than its genotypic equivalent, suggesting that apparent variation is caused not just by genes but also by environmental influences. For the majority of the traits, a small difference between PCV and GCV was observed (Table 2). For the majority of the recorded traits (Table 2), high heritability combined with high genetic gain as a percent of means was seen, indicating the majority of additive genetic influence in the determination of these traits. It also suggested that selecting for these characteristics might be beneficial for future clone improvement. However, significant heritability with modest genetic advance as a percent of mean was seen in leaf length and leaf breadth, demonstrating the importance of dominant genetic influences in the determination of these components and the need for careful selection to achieve the desired changes in the characteristics. Estimates of high heritability and high genetic gain both should be examined together to get a more accurate conclusion [23]. The heritable component of variation serves as the foundation for phenotypic performance-based selection. The mean tuber yield and disease parameters of high yielding (top 7) and low yielding (below 7) potato clones were shown in figure 1.

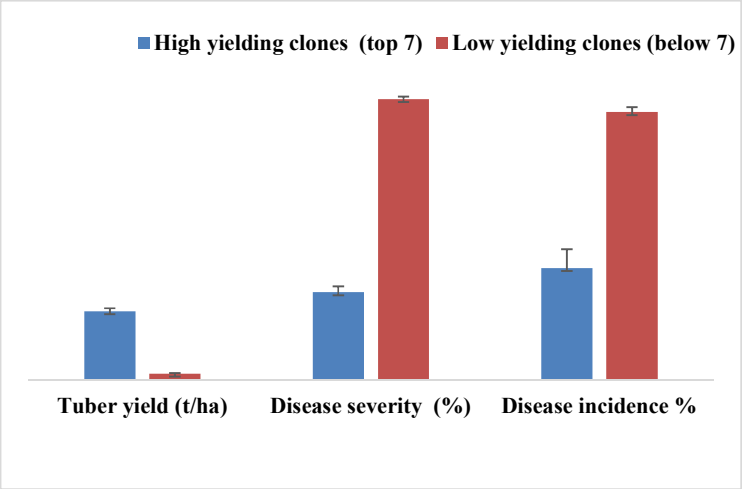

Figure 1. Tuber Yield and Late Blight Disease Parameters of High Yielding (Top 7) and Low Yielding (Below 7) Potato Clones at Rampur, Chitwan, Nepal during 2018-2019

The yield components of high yielding (top 7) and low yielding (below 7) potato clones were shown in figure 2.

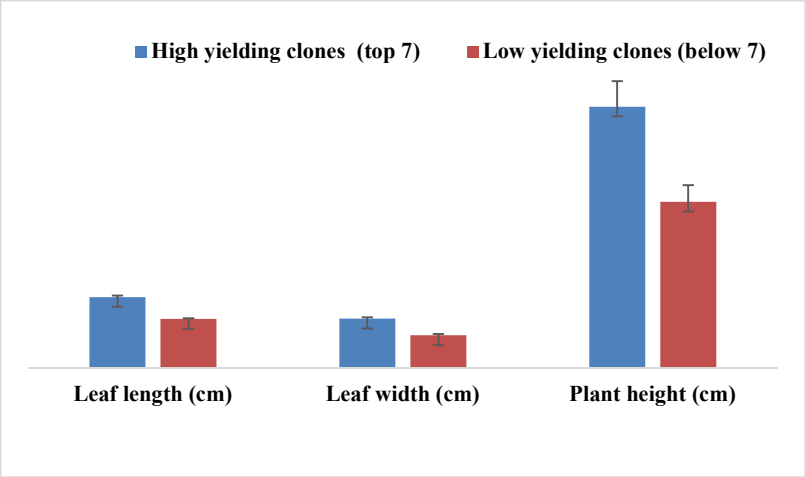

Figure 2. Yield Components of High Yielding (Top 7) and Low Yielding (Below 7) Potato Clones at Rampur, Chitwan, Nepal during 2018-2019

The genotypic correlation coefficients were generally greater than the phenotypic correlation coefficients. Higher genotypic correlations than phenotypic may be attributed to the environment altering or concealing the manifestation of these characteristics under examination as explained by [26]. The fact that genotypic correlation was larger than phenotypic correlation suggested an inherent link between different traits [23]. The positive and highly significant ($P < 0.01$) genotypic and phenotypic correlations were observed between all the disease parameters i.e. the three disease index, AUDPC, and disease incidence (Table 3). The strong negative and highly significant ($P < 0.01$) correlations were observed between tuber yield and disease parameters (PDI, AUDPC, and disease incidence) both at the genetic and phenotypic levels. The tuber yield was positively and significantly correlated with leaf length, leaf width, and plant height both at the genetic and phenotypic levels. Most of the yield attributing components like leaf length, leaf

width, and plant height except branches were negative and significantly correlated with all the recorded disease parameters (Table 3).

Table 3. Genotypic Correlation in Above Diagonal and Phenotypic Correlation in Below Diagonal of Late Blight Disease, Yield, and Yield Components in Potato Clones during 2018-2019 at Rampur, Chitwan, Nepal

Traits	PDI_I	PDI_II	PDI_III	AUDPC	DI%	LL (cm)	LW (cm)	PHT (cm)	Main stem	YLD (t/ha)
PDI_I		0.92**	0.80**	0.94**	0.84**	-0.62**	-0.66**	-0.53**	-0.29	-0.71**
PDI_II	0.92**		0.93**	0.99**	0.87**	-0.69**	-0.78**	-0.52**	-0.34*	-0.85**
PDI_III	0.79**	0.91**		0.96**	0.88**	-0.78**	-0.81**	-0.48**	-0.28	-0.92**
AUDPC	0.93**	0.99**	0.95**		0.89**	-0.72**	-0.77**	-0.51**	-0.31	-0.87**
DI%	0.81**	0.84**	0.86**	0.87**		-0.70**	-0.79**	-0.52**	-0.18	-0.84**
LL (cm)	-0.59**	-0.66**	-0.76**	-0.71**	-0.69**		0.85**	0.37*	0.34	0.86**
LW (cm)	-0.62**	-0.72**	-0.78**	-0.75**	-0.77**	0.85**		0.40*	0.30	0.86**
PHT (cm)	-0.51**	-0.49**	-0.47**	-0.51**	-0.51**	0.35*	0.40*		0.39*	0.43**
Main stem	-0.29	-0.33	-0.28	-0.32	-0.18	0.33	0.31	0.36*		0.23
YLD (t/ha)	- 0.69**	-0.81**	-0.91**	-0.85**	-0.82**	0.84**	0.84**	0.43*	0.22	

Note: PDI = percent disease index; I = 55 days after planting; II = 62 days after planting; III = 69 days after planting; AUDPC = area under disease progress curve; DI = disease incidence; LL = leaf length; LB = leaf breadth; PHT = plant height; YLD = yield; cm = centimeter; t/ha = ton per hectare; % = percentage; ** = significant at ≤ 0.01 p level; * = significant at ≤ 0.05 p level

There was a strong negative genotypic and phenotypic correlations among disease parameters, yield, and yield attributing components while positive correlations between yield and yield attributing components were observed which indicated that the tuber yield can be increased through a simple selection of the disease-resistant clones with these yield attributing components. The combined mean performance of potato clones to the late blight disease, yield, and yield components was shown in Table 4.

Table 4. Combined Mean Performance of Potato Clones to the Late Blight Disease and Yield and Yield Components during 2018-2019 at Rampur, Chitwan, Nepal

Clones	PDI (I)	PDI (II)	PDI (III)	AUDPC	r AUDPC	DI %	LL (cm)	LW (cm)	PHT (cm)	Main stem	Yield (t/ha)
CIP 304369.22	†27.30	48.56	70.58	780.66	0.49	74.26	4.98	3.55	15.74	2.36	7.90
CIP 392025.7	13.25	46.31	76.28	728.58	0.46	37.98	7.18	4.15	26.89	4.55	9.48
PRP 33971.11	43.23	66.30	88.24	1055.91	0.66	93.86	5.12	3.31	31.16	4.63	3.16
PRP 316368.2	56.61	77.78	96.74	1234.82	0.77	90.00	5.08	3.31	23.88	4.25	2.20
CIP 311350.2	67.06	74.84	91.86	1233.11	0.77	93.19	5.14	3.01	12.83	2.38	2.14
PRP 277072.122	12.28	18.28	24.27	295.38	0.18	31.51	6.65	5.14	31.83	3.75	23.65
CIP 392973.48	18.54	45.93	61.17	687.56	0.43	54.26	4.90	3.34	20.73	3.80	6.38
PRP 017072.108	16.57	45.24	66.69	699.88	0.43	58.14	5.34	3.08	26.83	2.91	3.78
PRP 146971.135	13.56	16.55	26.84	295.13	0.18	25.18	6.76	5.49	25.15	4.45	19.96
PRP 146971.117	20.39	25.04	33.32	421.03	0.26	26.45	7.57	5.27	22.18	4.71	22.85
CIP 311350.3	56.24	88.28	98.23	1305.66	0.83	94.72	4.77	2.76	13.90	2.80	1.89
PRP 336971.4	34.82	47.34	70.84	804.94	0.50	85.46	5.32	3.47	25.66	4.86	4.13
PRP 336971.8	46.47	73.84	95.26	1160.78	0.72	81.88	4.68	3.95	23.07	4.30	1.99
CIP 311350.13	48.10	74.31	94.06	1160.60	0.73	92.83	4.92	3.15	13.71	2.48	2.55
CIP 311546.25	25.45	44.80	56.35	685.01	0.43	73.33	7.13	4.01	24.45	4.50	7.74

Table 4. Continued

Clones	PDI (I)	PDI (II)	PDI (III)	AUDPC	r AUDPC	DI %	LL (cm)	LW (cm)	PHT (cm)	Main stem	Yield (t/ha)
CIP 311350.27	20.14	24.46	31.80	407.60	0.25	62.83	7.33	4.31	14.05	2.73	22.85
CIP 311622.9	12.98	15.76	23.05	274.25	0.17	18.93	7.37	4.70	32.11	3.75	27.71
PRP 367072.22	18.81	24.00	36.48	417.01	0.26	63.67	7.11	4.18	23.23	9.61	16.55
PRP 356971.3	50.03	73.34	96.19	1168.32	0.73	94.89	5.46	3.80	16.00	4.78	1.20
PRP 336971.2	34.42	55.49	84.38	905.40	0.57	85.42	5.95	4.02	27.82	5.40	3.43
CIP 311168.10	14.81	31.09	96.16	707.80	0.43	86.49	4.54	3.17	22.83	3.74	4.29
PRP 147072.27	15.00	20.99	30.27	359.22	0.22	46.98	7.78	5.37	30.09	4.99	21.10
PRP 146971.4	29.49	37.16	47.63	602.56	0.38	58.04	6.71	4.55	33.16	4.09	12.84
CIP 311187.4	29.16	38.85	63.38	688.08	0.43	73.93	4.02	3.01	16.33	3.99	3.24
PRP 146971.2	23.91	34.06	38.80	522.41	0.33	55.32	7.49	5.07	32.88	4.90	26.02
PRP 336971.9	33.31	44.41	68.15	765.34	0.48	61.50	5.32	3.91	24.88	4.65	4.91
PRP 136871.2	43.60	56.00	87.26	970.59	0.61	71.67	5.61	3.71	29.73	5.32	4.94
PRP 317072.8	15.52	35.51	45.30	527.32	0.33	52.26	6.19	3.81	40.85	5.01	16.52
CIP 395111.13	27.41	36.60	49.13	597.20	0.37	55.62	5.07	3.49	39.15	4.30	9.21
DESIRE (MR)	58.51	74.84	88.35	1152.18	0.74	88.99	4.83	2.64	24.60	4.20	4.64
Kuphri Jyoti (S)	59.67	79.46	98.00	1257.75	0.79	92.00	5.00	3.34	16.27	3.90	3.07
FL (HS)	54.83	80.70	94.50	1232.54	0.78	95.77	5.44	3.34	15.42	2.55	3.04
Grand Mean	32.54	48.63	66.55	784.52	0.49	68.04	5.83	3.85	24.29	4.21	9.54
CV, %	4.95	3.19	1.85	2.05	2.01	3.92	2.14	2.94	6.88	4.77	11.88

Note: †combined means of two replications; PDI = percent disease index; I = 55 days after planting; II = 62 days after planting; III = 69 days after planting; AUDPC = area under disease progress curve; r = relative; DI = disease incidence; LL = leaf length; LW = leaf width; PHT = plant height; CIP = Centro Internacional de la Papa (International potato center); PRP = potato research program; FL = Farmers local; MR = moderately resistant; S = susceptible; HS = highly susceptible; % = percentage; cm = centimeter; t/ha = ton per hectare

3.1. Relationships between Disease Severity (AUDPC) and Tuber Yield

The best fit, with R^2 = 72%, showed a substantial linear negative association (r = -0.85) between tuber yield and late blight severity (Figure 3). Consequently, as disease severity (AUDPC) increased, the yield was dropped. The projected linear regression line has a decreasing slope as well i.e. y = - 0.02x+26.72, with regression coefficient R^2 = 0.73, where 'y' denoted predicted crop yield (t/ha) of potato clones and 'x' stood for AUDPC value of late blight of potato (Figure 3).

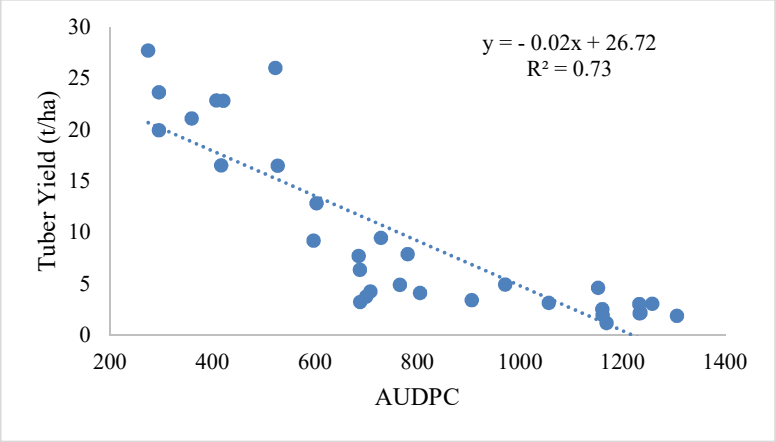

Figure 3. Relationship between Tuber Yield (t/ha) and AUDPC of Potato Late Blight at Rampur, Chitwan, Nepal during 2018-2019

3.2. Relationship between Leaf size and Tuber Yield

The best fit showed a substantial linear positive association (r =0.85) between tuber yield and leaf length (r = 0.84, R^2 = 71%) and leaf width (r = 0.83, R^2 = 70%) (Figure 4). Obviously, the yield increased as the leaf size grew. The predicted linear regression line was also displayed upward slope i.e. y = 0.11x + 4.81, with regression coefficient R^2 = 0.71, for leaf length and y = 0.08x + 3.11, with regression coefficient R^2 = 0.70 for leaf width where 'y' denoted predicted crop yield (t/ha) of potato clones and 'x' stood for leaf length and width in cm (Figure 4).

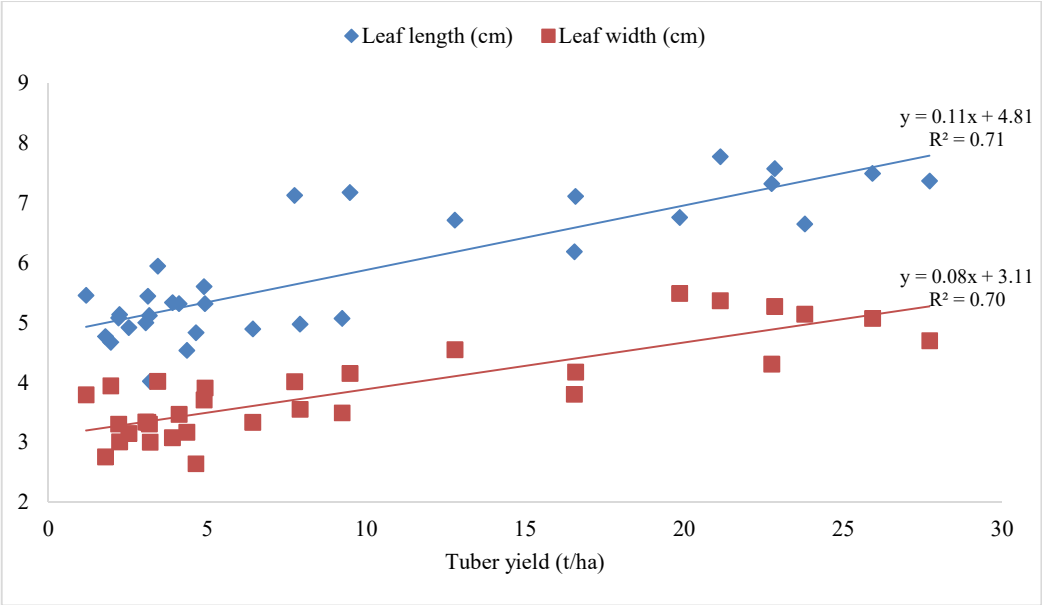

Figure 4. Relationship between Tuber Yield (t/ha) with Leaf Length and Width (cm) of Potato Clones at Rampur, Chitwan, Nepal during 2018-2019

The only optimal way to combat disease-related yield loss is to grow resistant genotypes [27]. The continuous screening of potato accessions for late blight resistance constitutes a major portion of potato breeding worldwide [28], [29]. Based on the disease parameters calculated over the years, six clones CIP 311622.9, PRP 277072.122, PRP 146971.135, PRP 147072.27, CIP 311350.27, and PRP 146971.117 (AUDPC= 274.25-421.03, PDI_III = 23.05-33.32%) showed resistant reaction (Table 4). None of the clones were found highly resistant to the late blight disease. The lower disease incidence ranged from 18.93-31.51% and was recorded in clones CIP 311622.9, PRP 146971.135, PRP 146971.117, and PRP 277072.122 respectively. Similar results were reported by [30], which indicated that potato clones CIP 311622.9, PRP 277072.122, PRP 146971.135 showed resistant to a moderately resistant reaction to late blight disease in different agro-ecological domains of the country. This result also corroborated with the findings of [31] which reported that potato exotic accessions have shown resistance to late blight in the South Asian region. Horizontal resistance to late blight is considered more durable and effective against all pathotypes of the pathogen [32], [33]. Environmental factors, on the other hand, might impact the manifestation of quantitative resistance [34], calling its stability across diverse testing or production circumstances into doubt. The leaf length was ranged from 4.02 to 7.78 cm. The higher

leaf length (7.78 cm) was recorded in clone PRP 147072.27. The leaf width was ranged from 2.64 to 5.49 cm and the higher leaf width (5.49 cm) was observed in PRP 146971.135. The plant height was ranged from 12.83 to 40.85 cm. The higher plant height (40.85 cm) was recorded in clone PRP 317072.8. The number of the main stem per plant was ranged from 2.36 to 9.61 and the highest main stem per plant (9.61) was found in PRP 367072.22 (Table 4). The tuber yield was ranged from 1.20 to 27.71 t/ha. The high yielding potato clones above 20 t/ha were CIP 311622.9 (27.71 t/ha), PRP 146971.2 (26.02 t/ha), PRP 277072.122 (23.65 t/ha), CIP 311350.27 (22.85 t/ha), PRP 146971.117 (22.85 t/ha), PRP 147072.27 (21.10 t/ha) and PRP 146971.135 (19.96 t/ha) respectively. These findings were in accordance with [35] for tuber yield and its attributing traits of CIP and PRP lines evaluated in various yield evaluation trials. Some elite potato accessions possessing multiple disease resistance genes were identified using DNA markers [29] [36]. The late blight resistant cultivars showed higher genetic variability compared to susceptible cultivars [37]. In contrast, the lowest genetic similarity was obtained among susceptible cultivars analyzed using RAPD markers [38].

4. Conclusion and Recommendation

We identified sufficient variability, high heritability, and genetic advance in the late blight disease and yield traits of potato clones. This will provides new insight into selecting superior and desire clones for further potato improvement. Potato clones CIP311622.9, PRP277072.122, PRP146971.135, PRP147072.27, CIP311350.27, and PRP146971.117 appear more resistant and produced higher tuber yield than other clones. The discovered late blight resistant potato clones might be used for national potato breeding efforts in Nepal to create late blight resistant potato cultivars.

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